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Sequence Listing could not be accepted.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Durreshwar Anjum

Timestamp: [year=2010; month=4; day=19; hr=16; min=4; sec=12; ms=154;]

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Reviewer Comments:

<210> 41

<211> 20

<212> DNA

<213> Synthetic reverse oligonucleotide primer HOM R2

<400> 41

gggcgattag ccattgatac

20

Numeric Identifier <213> can only be one of three choices, "Scientific name, i.e. Genus/species, Unknown or Artificial Sequence." For all sequences using "Unknown or Artificial sequence", for numeric identifier <213>, a mandatory feature is required to explain the source of the genetic material. The feature consists of <220>, which remains blank, and <223>, which states the source of the genetic material. Suggest using "Artificial sequence" for numeric identifier <213> and "Synthetic reverse oligonucleotide primer HOM R2" for numeric identifier <223> in the mandatory feature. Please check for similar errors and make all necessary changes.

Application No: 10562191 Version No: 2.0

Input Set:**Output Set:**

Started: 2010-04-14 16:37:33.107
Finished: 2010-04-14 16:37:43.950
Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 843 ms
Total Warnings: 44
Total Errors: 0
No. of SeqIDs Defined: 107
Actual SeqID Count: 107

Error code	Error Description
W 402	Undefined organism found in <213> in SEQ ID (4)
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W 402	Undefined organism found in <213> in SEQ ID (17)
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 402	Undefined organism found in <213> in SEQ ID (29)
W 402	Undefined organism found in <213> in SEQ ID (31)
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W 213	Artificial or Unknown found in <213> in SEQ ID (39)
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W 402	Undefined organism found in <213> in SEQ ID (41)
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W 213	Artificial or Unknown found in <213> in SEQ ID (48)
W 213	Artificial or Unknown found in <213> in SEQ ID (49)
W 402	Undefined organism found in <213> in SEQ ID (50)
W 402	Undefined organism found in <213> in SEQ ID (51)

Input Set:

Output Set:

Started: 2010-04-14 16:37:33.107

Finished: 2010-04-14 16:37:43.950

Elapsed: 0 hr(s) 0 min(s) 10 sec(s) 843 ms

Total Warnings: 44

Total Errors: 0

No. of SeqIDs Defined: 107

Actual SeqID Count: 107

Error code	Error Description
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W 402	Undefined organism found in <213> in SEQ ID (65)
W 402	Undefined organism found in <213> in SEQ ID (72)
W 402	Undefined organism found in <213> in SEQ ID (78) This error has occurred more than 20 times, will not be displayed
W 213	Artificial or Unknown found in <213> in SEQ ID (106)

SEQUENCE LISTING

<110> MASIGNANI, Vega
ARICO, Maria Beatrice

<120> VIRULENCE-ASSOCIATED ADHESINS

<130> 2300-20667

<140> 10562191

<141> 2010-04-14

<150> PCT/IB2004/002351

<151> 2004-06-25

<150> GB 0315022.4

<151> 2003-06-26

<160> 107

<170> PatentIn version 3.5

<210> 1

<211> 223

<212> PRT

<213> Haemophilus aegyptius

<400> 1

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			20					25					30		

Gln	Val	Lys	Lys	Asp	Glu	Leu	Ser	Glu	Leu	Lys	Lys	Gln	Val	Lys	Glu
		35					40					45			

Met	Asp	Ala	Ala	Ile	Asp	Gly	Ile	Leu	Asp	Asp	Asn	Ile	Ala	Tyr	Glu
	50					55					60				

Ala	Glu	Val	Asp	Ala	Lys	Leu	Asp	Gln	His	Ser	Ala	Ala	Leu	Gly	Arg
65					70					75					80

His	Thr	Asn	Arg	Leu	Asn	Asn	Leu	Lys	Thr	Ile	Ala	Glu	Lys	Ala	Lys
				85					90					95	

Gly	Asp	Ser	Ser	Glu	Ala	Leu	Asp	Lys	Ile	Glu	Ala	Leu	Glu	Glu	Gln
				100				105							110

Asn Asp Glu Phe Leu Ala Asp Ile Thr Ala Leu Glu Glu Gly Val Asp
115 120 125

Gly Leu Asp Asp Asp Ile Ala Gly Ile Gln Asp Asn Ile Ser Asp Ile
130 135 140

Glu Asp Asp Ile Asn Gln Asn Ser Ala Asp Ile Ala Thr Asn Thr Ala
145 150 155 160

Ala Ile Ala Thr His Thr Gln Arg Leu Asp Asn Leu Asp Asn Arg Val
165 170 175

Asn Asn Leu Asn Lys Asp Leu Lys Arg Gly Leu Ala Ala Gln Ala Ala
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Leu Asn Gly Leu Phe Gln Pro Tyr Asn Val Gly Lys Leu Asn Leu Thr
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210 215 220

<210> 2
<211> 338
<212> PRT
<213> Escherichia coli

<400> 2

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Glu Leu Ser Ala Ile Asn Ser Gly Met Ser Gln Ser Glu Ile Glu Gln
35 40 45

Lys Ile Thr Arg Phe Leu Glu Arg Thr Asp Asn Ser Pro Ala Ala Tyr
50 55 60

Thr Tyr Leu Thr Glu His His Tyr Ile Pro Ser Glu Thr Pro Asp Thr
65 70 75 80

Thr Gln Thr Pro Thr Val Gln Thr Asp Pro Asp Ala Gly Gln Lys Thr

85																90																95															
Val	Ala	Ala	Thr	Gly	Asp	Val	Gln	Thr	Thr	Ala	Arg	Tyr	Gln	Ser	Met																																
			100				105																																								
Ile	Asn	Ala	Arg	Gln	Ser	Ala	Val	Thr	Asp	Ala	Gln	Gln	Thr	Gln	Ile																																
			115				120																																								
Thr	Glu	Gln	Gln	Ala	Gln	Ile	Val	Ala	Thr	Gln	Lys	Thr	Leu	Ala	Ala																																
			130				135																																								
Thr	Gly	Asp	Thr	Gln	Asn	Thr	Ala	His	Tyr	Gln	Glu	Met	Ile	Asn	Ala																																
145				150													155																														
Arg	Leu	Ala	Ala	Gln	Asn	Glu	Ala	Asn	Gln	Arg	Thr	Ala	Thr	Glu	Gln																																
				165													170																														
Gly	Gln	Lys	Met	Asn	Ala	Leu	Thr	Thr	Asp	Val	Ala	Val	Gln	Gln	Gln																																
			180						185																																						
Asn	Glu	Arg	Thr	Gln	Tyr	Asp	Lys	Gln	Met	Gln	Ser	Leu	Ala	Gln	Glu																																
			195						200													205																									
Ser	Ala	Gln	Ala	His	Glu	Gln	Ile	Asp	Ser	Leu	Ser	Gln	Asp	Val	Thr																																
			210						215													220																									
Gln	Thr	His	Gln	Gln	Leu	Thr	Asn	Thr	Gln	Lys	Arg	Val	Ala	Asp	Asn																																
225				230													235																														
Ser	Gln	Gln	Ile	Asn	Thr	Leu	Asn	Asn	His	Phe	Ser	Ser	Leu	Lys	Asn																																
				245													250																														
Glu	Val	Asp	Asp	Asn	Arg	Lys	Glu	Ala	Asn	Ala	Gly	Thr	Ala	Ser	Ala																																
			260						265													270																									
Ile	Ala	Ile	Ala	Ser	Gln	Pro	Gln	Val	Lys	Thr	Gly	Asp	Val	Met	Met																																
			275						280													285																									
Val	Ser	Ala	Gly	Ala	Gly	Thr	Phe	Asn	Gly	Glu	Ser	Ala	Val	Ser	Val																																
			290						295													300																									
Gly	Thr	Ser	Phe	Asn	Ala	Gly	Thr	His	Thr	Val	Leu	Lys	Ala	Gly	Ile																																
305				310													315																														

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325 330 335

Ser Phe

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<211> 1588
<212> PRT
<213> Escherichia coli

<400> 3

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35 40 45

Phe Gly Ala Leu Ala Asn Ala Gly Asn Asp Asn Gly Gln Gly Val Asp
50 55 60

Tyr Gly Ser Gly Ser Ala Gly Asp Gly Trp Val Ala Ile Gly Lys Gly
65 70 75 80

Ala Lys Ala Asn Thr Phe Met Asn Thr Ser Gly Ser Ser Thr Ala Val
85 90 95

Gly Tyr Asp Ala Ile Ala Glu Gly Gln Tyr Ser Ser Ala Ile Gly Ser
100 105 110

Lys Thr His Ala Ile Gly Gly Ala Ser Met Ala Phe Gly Val Ser Ala
115 120 125

Ile Ser Glu Gly Asp Arg Ser Ile Ala Leu Gly Ala Ser Ser Tyr Ser
130 135 140

Leu Gly Gln Tyr Ser Met Ala Leu Gly Arg Tyr Ser Lys Ala Leu Gly
145 150 155 160

Lys	Leu	Ser	Ile	Ala	Met	Gly	Asp	Ser	Ser	Lys	Ala	Glu	Gly	Ala	Asn	
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Ala	Ile	Ala	Leu	Gly	Asn	Ala	Thr	Lys	Ala	Thr	Glu	Ile	Met	Ser	Ile	
			180					185					190			
Ala	Leu	Gly	Asp	Thr	Ala	Asn	Ala	Ser	Lys	Ala	Tyr	Ser	Met	Ala	Leu	
		195					200					205				
Gly	Ala	Ser	Ser	Val	Ala	Ser	Glu	Glu	Asn	Ala	Ile	Ala	Ile	Gly	Ala	
	210					215					220					
Glu	Thr	Glu	Ala	Ala	Glu	Asn	Ala	Thr	Ala	Ile	Gly	Asn	Asn	Ala	Lys	
225					230				235						240	
Ala	Lys	Gly	Thr	Asn	Ser	Met	Ala	Met	Gly	Phe	Gly	Ser	Leu	Ala	Asp	
				245					250						255	
Lys	Val	Asn	Thr	Ile	Ala	Leu	Gly	Asn	Gly	Ser	Gln	Ala	Leu	Ala	Asp	
			260					265					270			
Asn	Ala	Ile	Ala	Ile	Gly	Gln	Gly	Asn	Lys	Ala	Asp	Gly	Val	Asp	Ala	
		275					280					285				
Ile	Ala	Leu	Gly	Asn	Gly	Ser	Gln	Ser	Arg	Gly	Leu	Asn	Thr	Ile	Ala	
	290					295					300					
Leu	Gly	Thr	Ala	Ser	Asn	Ala	Thr	Gly	Asp	Lys	Ser	Leu	Ala	Leu	Gly	
305					310					315					320	
Ser	Asn	Ser	Ser	Ala	Asn	Gly	Ile	Asn	Ser	Val	Ala	Leu	Gly	Ala	Asp	
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Ser	Ile	Ala	Asp	Leu	Asp	Asn	Thr	Val	Ser	Val	Gly	Asn	Ser	Ser	Leu	
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Lys	Arg	Lys	Ile	Val	Asn	Val	Lys	Asn	Gly	Ala	Ile	Lys	Ser	Asp	Ser	
		355					360					365				
Tyr	Asp	Ala	Ile	Asn	Gly	Ser	Gln	Leu	Tyr	Ala	Ile	Ser	Asp	Ser	Val	
	370					375					380					
Ala	Lys	Arg	Leu	Gly	Gly	Gly	Ala	Ala	Val	Asp	Val	Asp	Asp	Gly	Thr	

385						390						395						400
Val	Thr	Ala	Pro	Thr	Tyr	Asn	Leu	Lys	Asn	Gly	Ser	Lys	Asn	Asn	Val			
				405					410					415				
Gly	Ala	Ala	Leu	Ala	Val	Leu	Asp	Glu	Asn	Thr	Leu	Gln	Trp	Asp	Gln			
				420					425					430				
Thr	Lys	Gly	Lys	Tyr	Ser	Ala	Ala	His	Gly	Thr	Ser	Ser	Pro	Thr	Ala			
				435					440					445				
Ser	Val	Ile	Thr	Asp	Val	Ala	Asp	Gly	Thr	Ile	Ser	Ala	Ser	Ser	Lys			
				450					455					460				
Asp	Ala	Val	Asn	Gly	Ser	Gln	Leu	Lys	Ala	Thr	Asn	Asp	Asp	Val	Glu			
465					470					475					480			
Ala	Asn	Thr	Ala	Asn	Ile	Ala	Thr	Asn	Thr	Ser	Asn	Ile	Ala	Thr	Asn			
				485					490					495				
Thr	Ala	Asn	Ile	Ala	Thr	Asn	Thr	Thr	Asn	Ile	Thr	Asn	Leu	Thr	Asp			
				500					505					510				
Ser	Val	Gly	Asp	Leu	Gln	Ala	Asp	Ala	Leu	Leu	Trp	Asn	Glu	Thr	Lys			
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Lys	Ala	Phe	Ser	Ala	Ala	His	Gly	Gln	Asp	Thr	Thr	Ser	Lys	Ile	Thr			
				530					535					540				
Asn	Val	Lys	Asp	Ala	Asp	Leu	Thr	Ala	Asp	Ser	Thr	Asp	Ala	Val	Asn			
545					550					555					560			
Gly	Ser	Gln	Leu	Lys	Thr	Thr	Asn	Asp	Ala	Val	Ala	Thr	Asn	Thr	Thr			
				565					570					575				
Asn	Ile	Ala	Asn	Asn	Thr	Ser	Asn	Ile	Ala	Thr	Asn	Thr	Thr	Asn	Ile			
				580					585					590				
Ser	Asn	Leu	Thr	Glu	Thr	Val	Thr	Asn	Leu	Gly	Glu	Asp	Ala	Leu	Lys			
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Trp	Asp	Lys	Asp	Asn	Gly	Val	Phe	Thr	Ala	Ala	His	Gly	Thr	Glu	Thr			
				610					615					620				

Thr Ser Lys Ile Thr Asn Val Lys Asp Gly Asp Leu Thr Thr Gly Ser
625 630 635 640

Thr Asp Ala Val Asn Gly Ser Gln Leu Lys Thr Thr Asn Asp Ala Val
645 650 655

Ala Thr Asn Thr Thr Asn Ile Ala Thr Asn Thr Thr Asn Ile Ser Asn
660 665 670

Leu Thr Glu Thr Val Thr Asn Leu Gly Glu Asp Ala Leu Lys Trp Asp
675 680 685

Lys Asp Asn Gly Val Phe Thr Ala Ala His Gly Asn Asn Thr Ala Ser
690 695 700

Lys Ile Thr Asn Ile Leu Asp Gly Thr Val Thr Ala Thr Ser Ser Asp
705 710 715 720

Ala Ile Asn Gly Ser Gln Leu Tyr Asp Leu Ser Ser Asn Ile Ala Thr
725 730 735

Tyr Phe Gly Gly Asn Ala Ser Val Asn Thr Asp Gly Val Phe Thr Gly
740 745 750

Pro Thr Tyr Lys Ile Gly Glu Thr Asn Tyr Tyr Asn Val Gly Asp Ala
755 760 765

Leu Ala Ala Ile Asn Ser Ser Phe Ser Thr Ser Leu Gly Asp Ala Leu
770 775 780

Leu Trp Asp Ala Thr Ala Gly Lys Phe Ser Ala Lys His Gly Thr Asn
785 790 795 800

Gly Asp Ala Ser Val Ile Thr Asp Val Ala Asp Gly Glu Ile Ser Asp
805 810 815

Ser Ser Ser Asp Ala Val Asn Gly Ser Gln Leu His Gly Val Ser Ser
820 825 830

Tyr Val Val Asp Ala Leu Gly Gly Gly Ala Glu Val Asn Ala Asp Gly
835 840 845

Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Asp Tyr Asp Asn
850 855 860

Val Gly Asp Ala Leu Asn Ala Ile Asp Thr Thr Leu Asp Asp Ala Leu
865 870 875 880

Leu Trp Asp Ala Asp Ala Gly Glu Asn Gly Ala Phe Ser Ala Ala His
885 890 895

Gly Lys Asp Lys Thr Ala Ser Val Ile Thr Asn Val Ala Asn Gly Ala
900 905 910

Ile Ser Ala Ala Ser Ser Asp Ala Ile Asn Gly Ser Gln Leu Tyr Thr
915 920 925

Thr Asn Lys Tyr Ile Ala Asp Ala Leu Gly Gly Asp Ala Glu Val Asn
930 935 940

Ala Asp Gly Thr Ile Thr Ala Pro Thr Tyr Thr Ile Ala Asn Ala Glu
945 950 955 960

Tyr Asn Asn Val Gly Asp Ala Leu Asp Ala Leu Asp Asp Asn Ala Leu
965 970 975

Leu Trp Asp Glu Thr Ala Asn Gly Gly Ala Gly Ala Tyr Asn Ala Ser
980 985 990

His Asp Gly Lys Ala Ser Ile Ile Thr Asn Val Ala Asn Gly Ser Ile
995 1000 1005

Ser Glu Asp Ser Thr Asp Ala Val Asn Gly Ser Gln Leu Asn Ala
1010 1015 1020

Thr Asn Met Met Ile Glu Gln Asn Thr Gln Ile Ile Asn Gln Leu
1025 1030 1035

Ala Gly Asn Thr Asp Ala Thr Tyr Ile Gln Glu Asn Gly Ala Gly
1040 1045 1050

Ile Asn Tyr Val Arg Thr Asn Asp Asp Gly Leu Ala Phe Asn Asp
1055 1060 1065

Ala	Ser	Ala	Gln	Gly	Val	Gly	Ala	Thr	Ala	Ile	Gly	Tyr	Asn	Ser	1070	1075	1080
Val	Ala	Lys	Gly	Asp	Ser	Ser	Val	Ala	Ile	Gly	Gln	Gly	Ser	Tyr	1085	1090	1095
Ser	Asp	Val	Asp	Thr	Gly	Ile	Ala	Leu	Gly	Ser	Ser	Ser	Val	Ser	1100	1105	1110
Ser	Arg	Val	Ile	Ala	Lys	Gly	Ser	Arg	Asp	Thr	Ser	Ile	Thr	Glu	1115	1120	1125
Asn	Gly	Val	Val	Ile	Gly	Tyr	Asp	Thr	Thr	Asp	Gly	Glu	Leu	Leu	1130	1135	1140
Gly	Ala	Leu	Ser	Ile	Gly	Asp	Asp	Gly	Lys	Tyr	Arg	Gln	Ile	Ile	1145	1150	1155
Asn	Val	Ala	Asp	Gly	Ser	Glu	Ala	His	Asp	Ala	Val	Thr	Val	Arg	1160	1165	1170
Gln	Leu	Gln	Asn	Ala	Ile	Gly	Ala	Val	Ala	Thr	Thr	Pro	Thr	Lys	1175	1180	1185
Tyr	Phe	His	Ala	Asn	Ser	Thr	Glu	Glu	Asp	Ser	Leu	Ala	Val	Gly	1190	1195	1200
Thr	Asp	Ser	Leu	Ala	Met	Gly	Ala	Lys	Thr	Ile	Val	Asn	Gly	Asp	1205	1210	1215
Lys	Gly	Ile	Gly	Ile	Gly	Tyr	Gly	Ala	Tyr	Val	Asp	Ala	Asn	Ala	1220	1225	1230
Leu	Asn	Gly	Ile	Ala	Ile	Gly	Ser	Asn	Ala	Gln	Val	Ile	His	Val	1235	1240	1245
Asn	Ser	Ile	Ala	Ile	Gly	Asn	Gly	Ser	Thr	Thr	Thr	Arg	Gly	Ala	1250	1255	1260
Gln	Thr	Asn	Tyr	Thr	Ala	Tyr	Asn	Met	Asp	Ala	Pro	Gln	Asn	Ser	1265	1270	1275
Val	Gly	Glu	Phe	Ser	Val	Gly	Ser	Ala	Asp	Gly	Gln	Arg	Gln	Ile			

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Thr Asn Val Ala Ala Gly Ser Ala Asp Thr Asp Ala Val Asn Val				
1295		1300		1305
Gly Gln Leu Lys Val Thr Asp Ala Gln Val Ser Gln Asn Thr Gln				
1310		1315		1320
Ser Ile Thr Asn Leu Asp Asn Arg Val Thr Asn Leu Asp Ser Arg				
1325		1330		1335
Val Thr Asn Ile Glu Asn Gly Ile Gly Asp Ile Val Thr Thr Gly				
1340		1345		1350
Ser Thr Lys Tyr Phe Lys Thr Asn Thr Asp Gly Val Asp Ala Ser				
1355		1360		1365
Ala Gln Gly Lys Asp Ser Val Ala Ile Gly Ser Gly Ser Ile Ala				
1370		1375		1380
Ala Ala Asp Asn Ser Val Ala Leu Gly Thr Gly Ser Val Ala Thr				
1385		1390		1395
Glu Glu Asn Thr Ile Ser Val Gly Ser Ser Thr Asn Gln Arg Arg				
1400		1405		1410
Ile Thr Asn Val Ala Ala Gly Lys Asn Ala Thr Asp Ala Val Asn				
1415		1420		1425
Val Ala Gln Leu Lys Ser Ser Glu Ala Gly Gly Val Arg Tyr Asp				
1430				